

SEQUENCE LISTING

<110> LUKYANOV, Sergei Anatolievich
SHAGIN, Dmitry Alexeevich
YANUSHEVICH, Yury Grigorievich
<120> FLUORESCENT PROTEINS AND CHROMOPROTEINS FROM NON-AEQUOREA HYDROZOA
SPECIES AND METHODS FOR USING SAME

<130> XXX

<160> 22

<170> PatentIn version 3.1

<210> 1

<211> 784

<212> DNA

<213> Phialidium sp.

<400> 1

gaactgataa aagaaaatcat catcatgtct agtggaggcac tggtttcca cggaaagatc	60
ccatatgttg tttagatggg gggaaatgtt gatggacaca cattctccat tagaggtaaa	120
ggttatggag atgcaggatgt tggtaaagt gatgcggcaat tcattctgcac aactggagat	180
gtaccagggtt catggtaaac tttagtaaca acacttactt atggtgacca atgcttcgccc	240
aaatatggtc cagaattaaa ggatttctac aagagttgca tgcctgaagg ctatgtgcag	300
gagcgtacaa tcacatgttga aggggacgga gtatttaaaa ctcgcgctga agttacattt	360
aaaaacggat ctgtttataaa ccgagtcaaa cttaatggac aaggatttaaa gaaagacgga	420
catgtgctt gaaagaatct tgaattcaat ttcacaccc tcatttttgcatttggggaa	480
gatcaggctt atcatggttt gaagtctgtt ttcaaaatata tgcatgagat tactggatca	540
aaagaagact tcattgttgc agaccacacc caaatgaaca caccattgg tggtgacca	600
gtccatgtcc ctgaataccca tcataataaca taccatgtca ctctcagcaa agatgttact	660
gatcacaggg ataacatgag cttgggtgaa accgtacggg ctgtggattt cagaaaaaca	720
tatctttaaa ttgtaaattt attttagtt gaaaaccttt tgtcacgata tataccttta	780
tttat	784

<210> 2

<211> 234

<212> PRT

<213> Phialidium sp.

<400> 2

Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val

1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys

20 25 30

19 May 2004

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
 115 120 125
 Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
 130 135 140
 Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
 145 150 155 160
 Ser Ala Phe Lys Ile Met His Glu Ile Thr Gly Ser Lys Glu Asp Phe
 165 170 175
 Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Pro
 180 185 190
 Val His Val Pro Glu Tyr His His Ile Thr Tyr His Val Thr Leu Ser
 195 200 205
 Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Val Glu Thr Val
 210 215 220
 Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
 225 230

<210> 3

<211> 705

<212> DNA

<213> Artificial sequence

<220>

<223> phiYFP-Y1 mutant sequence

<400> 3

atgccttagt gaggcactgtt gttccacgga aagatcccat atgttgttga gatggaggga	60
aatgttgatg gacacacatt ctccattttaga ggtaaaagggtt atggagatgc aagtgttgggt	120
aaagttgatg cccaaattcat ctgcacaact ggagatgtac cagttccatg gtcaacttta	180
gtacaacac ttacttatgg tgcacaatgc ttgcggccaaat atggtccaga attaaaggat	240
ttctacaaga gttgcatttgc tgaaggctat gtgcaggagc gtacaatcac atttgaaggg	300
gacggagttat ttaaaactcg cgctgaagtt acatttggaa acggatctgt ttataaccga	360
gtcaaactta atggacaagg atttaagaaa gacggacatg tgcttggaaa gaatcttgaa	420
ttcaatttca caccttcatttgc tctttacatt tggggagatc aggctaatca tggtttgaag	480
tctgcttca aaattatgca tgagattact ggatcaaaaag gagacttcat tggcagac	540
cacacccaaa tgaacacaccc cattgggtgtt ggaccagtcc atgtccctga ataccatcat	600
atgacatacc atgtcactct cagcaaaatgttactgatc acagggataaa catgagcttgc	660
tttggaaaccg tacgggctgtt ggattgcaga aaaacatatc tttaa	705

<210> 4

<211> 234

<212> PRT

<213> Artificial sequence

<220>

<223> phiYFP-Y1 mutant sequence

<400> 4

Met Pro Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val	
1 5 10 15	
Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys	
20 25 30	
Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys	
35 40 45	
Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu	
50 55 60	
Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp	
65 70 75 80	

IPEA/RU
AMENDED SHEET

<210> 5

<211> 705

<212> DNA

<213> Artificial sequence

<220>

<223> phiYFP-M0 mutant sequence

<400> 5

atgcctagtg	gagcactgtt	gttccacgg	aagatccat	atgttgttga	atggaggga	60
aatgtttagt	gacacacatt	ctccattaga	ggtaaaggtt	atggagatgc	aagtgttgg	120
aaagtttagt	cccaattcat	ctgcacaact	ggagatgtac	cagttccatg	gtcaacttta	180
gtacaacac	ttacttatgg	tgcacaatgc	ttcgccaaat	atggtccaga	attaaaggat	240
ttctacaaga	gttgcattgc	tgaaggctat	gtgcaggagc	gtacaatcac	atttgaaggg	300
gacggaaaact	ttaaaactcg	cgctgaagtt	acatttgaaa	acggatctgt	ttataaccga	360
gtcaaactta	atggacaagg	atttaagaaa	gacggacatg	tgcttggaaa	gaatcttcaa	420
ttcaatttca	cacctcatgg	tctttacatt	tggggagatc	aggctaatac	tggtttgaag	480
tctgcttca	aaattcgc	tgagattact	ggatcaaaag	gagacttcat	tgttgcagac	540
cacacccaaa	tgaacacacc	cattgggtgt	ggaccagtcc	atgtccctga	aaaccatcat	600
atgagctacc	atgtcaagct	cagcaaagat	gttactgtac	acagggataa	catgagcttg	660
aaggaaaccg	tacgggctgt	ggattgcaga	aaaacatatac	tttaa		705

<210> 6

<211> 234

<212> PRT

<213> Artificial sequence

<220>

<223> phiYFP-M0 mutant sequence

<400> 6

```

Met Pro Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
      5          10          15
1
Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
      20          25          30

```

19 May 2004

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
 35 40 45
 Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
 50 55 60
 Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
 65 70 75 80
 Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
 85 90 95
 Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
 100 105 110
 Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
 115 120 125
 Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
 130 135 140
 Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
 145 150 155 160
 Ser Ala Phe Lys Ile Arg His Glu Ile Thr Gly Ser Lys Gly Asp Phe
 165 170 175
 Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Pro
 180 185 190
 Val His Val Pro Glu Asn His His Met Ser Tyr His Val Lys Leu Ser
 195 200 205
 Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
 210 215 220
 Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
 225 230

<210> 7

<211> 705

<212> DNA

<213> Artificial sequence

<220>

<223> phiYFP-M1 mutant sequence

<400> 7

atgtctagtg	gagcactgtt	gttccacgga	aagatccccat	atgttgtga	gatggaggga	60
aatgttgatg	gacacacatt	ctccattaga	ggtaaagggt	atggagatgc	aagtgttgg	120
aaagttgtatg	cccaattcat	ctgcacaact	ggagatgtac	cagttccatg	gtcaacttta	180
gtaacaacac	ttacttatgg	tgcacaatgc	ttcgccaaat	atggtccaga	attaaaggat	240
ttctacaaga	gttgcattgcc	tgatggctat	gtgcaggagc	gtacaatcac	atttgaaggg	300
gacggaaaact	ttaaaactcg	cgctgaagtt	acatttggaaa	acggatctgt	ttataaccga	360
gtcaaactta	atggacaagg	attnaagaaa	gacggacatg	tgcttggaaa	gaatcttgaa	420
tccaatttca	cacccatttg	tctttacatt	tggggagatc	aggctaatac	tggtttgaag	480
tctgctttca	aaatttgcca	tgagattact	ggatcaaaag	gagacttcat	tgttgcagac	540
cacacccaaa	tgaacacacc	cattggtggt	ggaccagtcc	atgtccctga	ataccatcat	600
atgagctacc	atgtcaagct	cagcaaagat	gttactgatc	acagggataa	catgagcttg	660
aaggaaaccg	tacgggctgt	ggattgcaga	aaaacataatc	tttaa		705

<210> 8

<211> 234

<212> PRT

<213> Artificial sequence

<220>

<223> phiYFP-M1 mutant sequence

<400> 8

Thr	Thr	Gly	Asp	Val	Pro	Val	Pro	Trp	Ser	Thr	Leu	Val	Thr	Thr	Leu
50															
Thr	Tyr	Gly	Ala	Gln	Cys	Phe	Ala	Lys	Tyr	Gly	Pro	Glu	Leu	Lys	Asp
65															
Phe	Tyr	Lys	Ser	Cys	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile
	85									90					95
Thr	Phe	Glu	Gly	Asp	Gly	Asn	Phe	Lys	Thr	Arg	Ala	Glu	Val	Thr	Phe
	100								105						110
Glu	Asn	Gly	Ser	Val	Tyr	Asn	Arg	Val	Lys	Leu	Asn	Gly	Gln	Gly	Phe
	115							120							125
Lys	Lys	Asp	Gly	His	Val	Leu	Gly	Lys	Asn	Leu	Glu	Phe	Asn	Phe	Thr
	130						135								140
Pro	His	Cys	Leu	Tyr	Ile	Trp	Gly	Asp	Gln	Ala	Asn	His	Gly	Leu	Lys
	145					150				155					160
Ser	Ala	Phe	Lys	Ile	Arg	His	Glu	Ile	Thr	Gly	Ser	Lys	Gly	Asp	Phe
	.					165				170					175
Ile	Val	Ala	Asp	His	Thr	Gln	Met	Asn	Thr	Pro	Ile	Gly	Gly	Pro	
	180							185							190
Val	His	Val	Pro	Glu	Asn	His	His	Met	Ser	Tyr	His	Val	Lys	Leu	Ser
	195							200							205
Lys	Asp	Val	Thr	Asp	His	Arg	Asp	Asn	Met	Ser	Leu	Lys	Glu	Thr	Val
	210							215							220
Arg	Ala	Val	Asp	Cys	Arg	Lys	Thr	Tyr	Leu						
	225							230							

<210> 7
<211> 705
<212> DNA
<213> Artificial sequence
<220>
<223> phiYFP-M1 mutant of
<400> 7

atgtcttagt gggactgtt gttccacgga aagatcccattt atgttgttga gatggaggggaaatgttgatg gacacacattt ctccattttaga gtaaaagggtt atggagatgc aagtgttggtaaagttgtat cccaaattcat ctgcacaactt ggagatgtac cagttccatgttcaactttttaaacaacac ttacttatgg tgcacaatgc ttgcacaat atggtccaga attaaaggatttctacaaga gttgcatttgc ttatggctat gtgcaggagc gtacaatcac atttgaaggggacggaaactt taaaactcg cgctgaagttt acatttgaaa acggatctgt ttataaccgatgtcaaactta atggacaagg atttaagaaa gacggacatgtt tgcttggaaa gaatcttggaaatccaatttca cacctcatttgc ttttacattt tggggagatc aggctaattca tggtttgaag

tctgcttca aaatttgc	ca tgagattact ggatcaaaag gagacttc	at tttgcagac	540
cacacccaaa tgaacacacc cattgggt	gg accagtcc atgtccctga ataccatcat		600
atgagctacc atgtcaagct cagcaaagat gttactgatc acaggataa catgagctt			660
aaggaaaccg tacgggctgt ggattgcaga aaaacatatc tttaa			705

<210> 8
<211> 234
<212> PRT
<213> Artificial sequence
<220>
<223> phiYFP-M1 mutant of the phiYFP
<400> 8

Met Ser Ser Gly Ala Leu Leu Phe His	Gly Lys Ile Pro Tyr Val Val		
1	5	10	15
Glu Met Glu Gly Asn Val Asp Gly His	Thr Phe Ser Ile Arg Gly Lys		
20	25	30	
Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys			
35	40	45	
Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu			
50	55	60	
Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp			
65	70	75	80
Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile			
85	90	95	
Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe			
100	105	110	
Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe			
115	120	125	
Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr			
130	135	140	
Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys			
145	150	155	160
Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe			
165	170	175	
Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Pro			
180	185	190	
Val His Val Pro Glu Tyr His His Met Ser Tyr His Val Lys Leu Ser			
195	200	205	
Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val			
210	215	220	

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225 230

<210> 9
<211> 705
<212> DNA
<213> Artificial sequence
<220>
<223> humanized version of the phiYFP-M1
<400> 9

atgagcagcg gcgcctgtct gttccacggc aagatcccct acgtggtgga gatggaggc 60
aatgtggatg gccacacaccc cagcatccgc ggcaaggcgt acggcgatgc cagcgtggc 120
aaggtggatg cccagttcat ctgcaccacc ggcgatgtgc ccgtgccctg gagcacccctg 180
gtgaccaccc tgacctacgg cgcccagtgc ttgcgccaagt acggccccga gctgaaggat 240
ttctacaaga gctgcattgcc cgtggctac gtgcaggagc gcaccatcac cttcgaggc 300
gatggcaatt tcaagaccccg cgccgaggtg accttcgaga atggcagcgt gtacaatcgc 360
gtgaagctga atggccaggg cttcaagaag gatggccacg tgctggcaa gaatctggag 420
ttcaatttca ccccccactg cctgtacatc tggggcgatc aggccaatca cggcctgaag 480
agcgccttca agatctgcca cgagatcacc ggcagcaagg gcgatttcat cgtggccgt 540
cacacccaga tgaataaccc catcggcgcc ggccccgtgc acgtgcccga gtaccaccac 600
atgagctacc acgtgaagct gagcaaggat gtgaccgatc accggcgataa tatgagcctg 660
aaggagaccc tgcgccgt ggattgcccgc aagacctacc tgtga 705

<210> 10
<211> 234
<212> PRT
<213> Artificial sequence
<220>
<223> humanized version of the phiYFP-M1
<400> 10

Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
1 5 10 15
Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20 25 30
Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35 40 45
Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
 65 70 75 80
 Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
 85 90 95
 Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
 100 105 110
 Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
 115 120 125
 Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
 130 135 140
 Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
 145 150 155 160
 Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
 165 170 175
 Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Pro
 180 185 190
 Val His Val Pro Glu Tyr His His Met Ser Tyr His Val Lys Leu Ser
 195 200 205
 Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
 210 215 220
 Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
 225 230

<210> 11
 <211> 1047
 <212> DNA
 <213> hydromedusa 1 from sub-order Anthomedusae
 <400> 11

cttttcttaa	aaagaattca	aaaaggacgg	tttactagac	atacttatac	agctttactt	60
ataaaaggaaag	aaatgaatgt	gatgcgttac	aacagaggat	tctgcagagt	tttgcaaaat	120
ggtgtcaaaa	attacgttc	tagaaattgc	agtacggaag	aaaaaccgt	catacttgtt	180
gcaatgacag	aaacatttca	aaaaaaatttgc	ccatataagt	tagaatttgg	tggagatgtt	240
gatggggaaa	catttaaggt	tatttgttag	ggcggtgggg	atgcaaccac	tggtgtaatt	300
gaaggaaaat	atgtttgtac	agaaggagaa	gttccttattt	catgggtttc	gctcatcacc	360
tcattaagtt	atggtgcgaa	atgtttgtt	cgatatccaa	atgaaataaa	tgattttttc	420
aaaagtactt	ttccttctgg	atatcatcaa	gaaagaaaaaa	ttacatatga	aatgtatgtt	480
gttttagaaa	cagcagctaa	aattactatg	gaaagtgggt	caatagtgaa	tagaataaaat	540
gtgaaaggca	caggcttcga	taaagatggt	catgtatgcc	aaaaaaatct	tgaatccccc	600
cctccttcga	caacatatgt	tggtccccag	ggagaaggta	ttcgaatcat	ctatagaaac	660
atctatccaa	caaaagatgg	tcactatgtt	gttgccgaca	cacagcaagt	aaatcgacca	720

at tagagcac a aggaacatc agctatccca acatatcatc acattaaatc gaaaaggat	780
c tttcaacag at ccagaaga aaataaaagat catattatca tcaaagaaac caactgcgca	840
t ttgacgctg at ttttctta agattccga ttgcattcaa gattaaaaaa ctaaataaag	900
a taggtaaaaa aaaatatgtc ttgtatgtta catacagtat tgatataagc ttcaaagaaa	960
tatatttca aataaaacttt ataaaattag gaatcttga atatataaac taaaccttt	1020
at ttgtagaa taaaaataat taaagac	1047

<210> 12
<211> 262
<212> PRT
<213> hydromedusa 1 from sub-order Anthomedusae
<400> 12

Met Asn Val Met Arg Tyr Asn Arg Gly Phe Cys Arg Val Leu Gln Asn			
1	5	10	15
Gly Val Lys Asn Leu Arg Ser Arg Asn Cys Ser Thr Glu Glu Lys Pro			
20	25	30	
Val Ile Leu Gly Ala Met Thr Glu Thr Phe Gln Lys Lys Leu Pro Tyr			
35	40	45	
Lys Leu Glu Leu Asp Gly Asp Val Asp Gly Gln Thr Phe Lys Val Ile			
50	55	60	
Gly Glu Gly Val Gly Asp Ala Thr Thr Gly Val Ile Glu Gly Lys Tyr			
65	70	75	80
Val Cys Thr Glu Gly Glu Val Pro Ile Ser Trp Val Ser Leu Ile Thr			
85	90	95	
Ser Leu Ser Tyr Gly Ala Lys Cys Phe Val Arg Tyr Pro Asn Glu Ile			
100	105	110	
Asn Asp Phe Phe Lys Ser Thr Phe Pro Ser Gly Tyr His Gln Glu Arg			
115	120	125	
Lys Ile Thr Tyr Glu Asn Asp Gly Val Leu Glu Thr Ala Ala Lys Ile			
130	135	140	
Thr Met Glu Ser Gly Ala Ile Val Asn Arg Ile Asn Val Lys Gly Thr			
145	150	155	160
Gly Phe Asp Lys Asp Gly His Val Cys Gln Lys Asn Leu Glu Ser Ser			
165	170	175	
Pro Pro Ser Thr Thr Tyr Val Val Pro Glu Gly Glu Gly Ile Arg Ile			
180	185	190	
Ile Tyr Arg Asn Ile Tyr Pro Thr Lys Asp Gly His Tyr Val Val Ala			
195	200	205	
Asp Thr Gln Gln Val Asn Arg Pro Ile Arg Ala Gln Gly Thr Ser Ala			
210	215	220	

Ile Pro Thr Tyr His His Ile Lys Ser Lys Val Asp Leu Ser Thr Asp
 225 230 235 240
 Pro Glu Glu Asn Lys Asp His Ile Ile Ile Lys Glu Thr Asn Cys Ala
 245 250 255
 Phe Asp Ala Asp Phe Ser
 260

<210> 13
<211> 1089
<212> DNA
<213> hydromedusa 2 from sub-order Anthomedusae
<400> 13

atcattcgct gatacgaagt gaaagtagcg tttgctgaaa gcttcctgga attgctccta	60
cgtatcttga aagttgctcc tacgctccaa ctgtttgtt caaaaatggaa ggtggtccag	120
cattatttca atccgatatg acattcaaga tcttcatcga tggagtggtg aatgatcaga	180
aattcacgat aatcgcatatg ggatcgcca aattccccca tggacttc aacgtgcattg	240
ctgtgtgcga aaccgggaaa ctcccaatgt catggaaacc tatttgtcac cttatccaa	300
acggggagcc attcttgca aaatatccca atggcatcag ccatttgca caggagtgc	360
ttccagaagg attaacaatt gatcgaacag tcagattcga aaatgacggc actatgacgt	420
ctcaccacac ctatgatggc gacggcacct gtgtcatttc caggataacc gttaaattgtg	480
acggatttca acctgatggc ccaatcatga aagaccagct tggtatgtc ctgccaactg	540
agacacatat gttccctcat gggtccaatg ctgtcagaca attgtctac attggcttca	600
cgacagctga tggtggtctc atgatgtcac attttgattc gaaattgaca ttcaatggtt	660
cgagagcaat caagattcct ggacccatt tcgttactgt gataatcaaa cagatgaaag	720
atacaagcga caagcgtgat catgtgtgc aacgtgaagt cacctacgct cactcagttc	780
cacgcacatcac ttctgctatc taaacatcat tcttaaaagg ggaacatgca catcatactt	840
cagtgtgagg gtcagtgtga gggtcttag atgtcaattt gtcgcagggtg tcacacggcg	900
tcgttttagat gttgaaggac gaaatgcgac aaagagatta atagagactc atattttat	960
gtagaatcga ttcatcaggc ccattggtaa ctttttggt attttatcat cttattattt	1020
tattggcact ttgttatat tttgtatgta atgttaaac aattgtgaa aatacatgtc	1080
aagaacttg	1089

<210> 14
<211> 232
<212> PRT
<213> hydromedusa 2 from sub-order Anthomedusae
<400> 14

Met Glu Gly Gly Pro Ala Leu Phe Gln Ser Asp Met Thr Phe Lys Ile

Phe Ile Asp Gly Val Val Asn Asp Gln Lys Phe Thr Ile Ile Ala Asp
 20 25 30
 Gly Ser Ser Lys Phe Pro His Gly Asp Phe Asn Val His Ala Val Cys
 35 40 45
 Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile
 50 55 60
 Gln Tyr Gly Glu Pro Phe Phe Ala Lys Tyr Pro Asn Gly Ile Ser His
 65 70 75 80
 Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Thr Ile Asp Arg Thr Val
 85 90 95
 Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu
 100 105 110
 Asp Gly Thr Cys Val Ile Ser Arg Ile Thr Val Asn Cys Asp Gly Phe
 115 120 125
 Gln Pro Asp Gly Pro Ile Met Lys Asp Gln Leu Val Asp Ile Leu Pro
 130 135 140
 Thr Glu Thr His Met Phe Pro His Gly Ser Asn Ala Val Arg Gln Leu
 145 150 155 160
 Cys Tyr Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His
 165 170 175
 Phe Asp Ser Lys Leu Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro
 180 185 190
 Gly Pro His Phe Val Thr Val Ile Ile Lys Gln Met Lys Asp Thr Ser
 195 200 205
 Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser
 210 215 220
 Val Pro Arg Ile Thr Ser Ala Ile
 225 230

<210> 15
<211> 699
<212> DNA
<213> Artificial sequence
<220>
<223> S3-2 mutant of the hm2CP
<400> 15

atggaaggtg gtc	caggcatt atttcaatcc	gacatgacat tcaagatctt	catcgatgga	60
gtggtaatg gtc	agaaatt cacgatagtc	gcagatggat cgtccaaatt	ccccatgg	120
gacttcaacg tacatgctgt	gtgcgaaacc gggaaactcc	aatgtcatg gaaaccatt		180
tgtcacctt	tccaatacgg ggagccattc	tttgcaagat atcccaacgg	catcagccat	240

tttgcacagg	agtgcattcc	agaaggatta	tcaattgatc	gaacagtcag	attcgaaaat	300
gacggcacta	tgacgtctca	ccacacctat	gagttggacg	gcaccctgtgt	cgttccagg	360
ataaccgtta	attgtgacgg	atttcaacct	gatggaccaa	tcatgagaga	ccagcttgtt	420
gatatcctgc	caaacgagac	acatatgttc	cctcatggac	ccaatgctgt	cagacaattg	480
gctttcatag	gcttcacgac	agctgatggt	ggtctcatga	tgtcacattt	tgattcggaa	540
atgacattca	atggttcgag	agcaatcaag	attcctggac	ctcattcgt	cactaccata	600
accaaacaga	tgaaagatac	aagcgacaag	cgtgatcatg	tgtgtcagcg	ggaagtcacc	660
tacgctca	cagttccacg	catcacttct	gctatctaa			699

<210> 16
 <211> 232
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> S3-2 mutant of the hm2CP
 <400> 16

Met	Glu	Gly	Gly	Pro	Ala	Leu	Phe	Gln	Ser	Asp	Met	Thr	Phe	Lys	Ile
1															15
Phe	Ile	Asp	Gly	Val	Val	Asn	Gly	Gln	Lys	Phe	Thr	Ile	Val	Ala	Asp
				20					25						30
Gly	Ser	Ser	Lys	Phe	Pro	His	Gly	Asp	Phe	Asn	Val	His	Ala	Val	Cys
					35			40							45
Glu	Thr	Gly	Lys	Leu	Pro	Met	Ser	Trp	Lys	Pro	Ile	Cys	His	Leu	Ile
				50			55				60				
Gln	Tyr	Gly	Glu	Pro	Phe	Phe	Ala	Arg	Tyr	Pro	Asn	Gly	Ile	Ser	His
				65			70			75					80
Phe	Ala	Gln	Glu	Cys	Phe	Pro	Glu	Gly	Leu	Ser	Ile	Asp	Arg	Thr	Val
					85				90						95
Arg	Phe	Glu	Asn	Asp	Gly	Thr	Met	Thr	Ser	His	His	Thr	Tyr	Glu	Leu
					100			105							110
Asp	Gly	Thr	Cys	Val	Val	Ser	Arg	Ile	Thr	Val	Asn	Cys	Asp	Gly	Phe
					115			120				125			
Gln	Pro	Asp	Gly	Pro	Ile	Met	Arg	Asp	Gln	Leu	Val	Asp	Ile	Leu	Pro
					130			135			140				
Asn	Glu	Thr	His	Met	Phe	Pro	His	Gly	Pro	Asn	Ala	Val	Arg	Gln	Leu
				145			150			155					160
Ala	Phe	Ile	Gly	Phe	Thr	Thr	Ala	Asp	Gly	Gly	Leu	Met	Met	Ser	His
					165				170						175
Phe	Asp	Ser	Lys	Met	Thr	Phe	Asn	Gly	Ser	Arg	Ala	Ile	Lys	Ile	Pro
					180			185				190			

Gly Pro His Phe Val Thr Thr Ile Thr Lys Gln Met Lys Asp Thr Ser
195 200 205
Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser
210 215 220
Val Pro Arg Ile Thr Ser Ala Ile
225 230

<210> 17
<211> 705
<212> DNA
<213> Artificial sequence
<220>
<223> phiYFP-M1G1 mutant, derived from humanized version of the phiYFP-M1
<400> 17

atgtccagcg gcccctgct gttccacggc aagatcccct acgtggtgga gatggaggc 60
aatgtggatg gccacacacctt cagcatccgc ggcaagggtc acggcgatgc cagcgtggc 120
aagggtggatg cccagttcat ctgcaccacc ggcgatgtgc ccgtgccctg gagcaccctg 180
gtgaccaccc tgcctacgg cgcccagtgc ttgcgccaagt acggccccga gctgaaggat 240
ttctacaaga gctgcattgcc cgatggctac gtgcaggagc gcaccatcac ctgcgaggc 300
gatggcaatt tcaagaccccg cgccgaggtg accttcgaga atggcagcgt gtacaatcgc 360
gtgaagctga atggccaggg cttcaagaag gatggccacg tgctggcaa gaatctggag 420
ttcaatttca ccccccactg ccagtacatc tggggcgatc aggccaatca cggcctgaag 480
agcgccttca agatctgcca cgagatcacc ggcagcaagg gcatgttcat cgtggccat 540
cacacccaga tgaataacccc catcgccggc ggccccgtgc acgtgcccga gtaccaccac 600
atgagcaccc acgtgaagct gagcaaggat gtgaccgatc accgcgataa tatgagcctg 660
aaggagaccc tgccgcgcgt ggattgccga acagcctacc tgtga 705

<210> 18
<211> 234
<212> PRT
<213> Artificial sequence
<220>
<223> phiYFP-M1G1 mutant, derived from humanized version of the phiYFP-M1
<400> 18

Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
 20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
 35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
 50 55 60

Ser Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
 65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
 85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
 100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
 115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
 130 135 140

Pro His Cys Gln Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
 145 150 155 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
 165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Pro
 180 185 190

Val His Val Pro Glu Tyr His His Met Ser Thr His Val Lys Leu Ser
 195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
 210 215 220

Arg Ala Val Asp Cys Arg Thr Ala Tyr Leu
 225 230

<210> 19

<211> 705

<212> DNA

<213> Artificial sequence

<220>

<223> phiYFP-M1C1 mutant, derived from humanized version of the phiYFP-M1

<400> 19

atgtccagcg	gccccagct	gttccacggc	aagatcccct	acgtggtgga	gatggagggc	60
aatgtggatg	gccacacctt	cagcatccgc	ggcaagggt	acggcgatgc	cagcgtggc	120
aaggtggatg	cccagttcat	ctgcaccacc	ggcgatgtgc	ccgtgccctg	gagcaccctg	180

gtgaccaccc	tgtcctgggg	cgcggcgtgc	ttcgccaagt	acggccccga	gctgaaggat	240
ttctacaaga	gctgcattgcc	cgatggctac	gtgcaggagc	gcaccatcac	cttcgagggc	300
gatggcaatt	tcaagacccg	cgccgagggtg	accttcgaga	atggcagcgt	gtacaatcgc	360
gtgaagctga	aaggccaggg	cttcaagaag	gatggccacg	tgctggcaa	aatctggag	420
ttcaatttca	ccccccacta	ccagtacatc	tggggcgatc	aggccaatca	cggcctgaag	480
agcgcttca	agatctgca	cgagatcacc	ggcagtaagg	gcgatttcat	cgtggccgat	540
cacacccaga	tgaataacccc	catcggcggc	ggcccccgtgc	acgtgcccga	gtaccaccac	600
atgagcaccc	acgtgaagct	gagcaaggat	gtgaccgatc	accgcgataa	tatgagcctg	660
aaggagacct	tgcgcgccgt	ggattgccgc	aagacctacc	tgtga		705

<210> 20

<211> 234

<212> PRT

<213> Artificial sequence

<220>

<223> phiYFP-M1C1 mutant, derived from humanized version of the phiYFP-M1

<400> 20

Met	Ser	Ser	Gly	Ala	Gln	Leu	Phe	His	Gly	Lys	Ile	Pro	Tyr	Val	Val
1				5					10					15	
Glu	Met	Glu	Gly	Asn	Val	Asp	Gly	His	Thr	Phe	Ser	Ile	Arg	Gly	Lys
					20				25					30	
Gly	Tyr	Gly	Asp	Ala	Ser	Val	Gly	Lys	Val	Asp	Ala	Gln	Phe	Ile	Cys
				35			40					45			
Thr	Thr	Gly	Asp	Val	Pro	Val	Pro	Trp	Ser	Thr	Leu	Val	Thr	Thr	Leu
	50				55					60					
Ser	Trp	Gly	Ala	Gln	Cys	Phe	Ala	Lys	Tyr	Gly	Pro	Glu	Leu	Lys	Asp
	65				70				75			80			
Phe	Tyr	Lys	Ser	Cys	Met	Pro	Asp	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile
					85			90				95			
Thr	Phe	Glu	Gly	Asp	Gly	Asn	Phe	Lys	Thr	Arg	Ala	Glu	Val	Thr	Phe
				100			105					110			
Glu	Asn	Gly	Ser	Val	Tyr	Asn	Arg	Val	Lys	Leu	Lys	Gly	Gln	Gly	Phe
				115			120				125				
Lys	Lys	Asp	Gly	His	Val	Leu	Gly	Lys	Asn	Leu	Glu	Phe	Asn	Phe	Thr
					130		135				140				
Pro	His	Tyr	Gln	Tyr	Ile	Trp	Gly	Asp	Gln	Ala	Asn	His	Gly	Leu	Lys
	145				150				155			160			
Ser	Ala	Phe	Lys	Ile	Cys	His	Glu	Ile	Thr	Gly	Ser	Lys	Gly	Asp	Phe
				165			170				175				

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
 180 185 190
 Val His Val Pro Glu Tyr His His Met Ser Thr His Val Lys Leu Ser
 195 200 205
 Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Leu
 210 215 220
 Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
 225 230

<210> 21
 <211> 699
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> humanized version of the S3-2 mutant
 <400> 21

atggagggcg gccccgcctt gttccagagc gacatgacct tcaaaatctt catcgacggc	60
gtggtaacg gccagaagtt caccatgtg gccgacggca gcagcaagtt ccccccacggc	120
gacttcaacg tgcacgccgt gtgcgagacc ggcaagctgc ccatgagctg gaagcccatc	180
tgcacactga tccagtacgg cgagcccttc ttgcggccgtt accccaacgg catcagccac	240
ttcgccccagg agtgcttccc cgagggcctg agcategacc gcaccgtgctg cttcgagaac	300
gacggcacca tgaccagcca ccacacccatc gagctggacg gcacccgtgt ggtgagccgc	360
atcaccgtga actgcgacgg cttccagccc gacggcccca tcatgcgcga ccagctggtg	420
gacatcctgc ccaacgagac ccacatgttc ccccacggcc ccaacgccgt gcgccagctg	480
gccttcatcg gcttcaccac cgccgacggc ggcctgtatga tgagccactt cgacagcaag	540
atgaccttca acggcagccg cgccatcaag atccccggcc cccacttcgt gaccaccatc	600
accaagcaga tgaaggacac cagcgacaag cgcgaccacg tgtgccagcg cgaggtgacc	660
tacgcccaca gcgtgccccg catcaccagc gccatctga	699

<210> 22
 <211> 232
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> humanized S3-2 mutant
 <400> 22

Met Glu Gly Gly Pro Ala Leu Phe Gln Ser Asp Met Thr Phe Lys Ile

Phe Ile Asp Gly Val Val Asn Gly Gln Lys Phe Thr Ile Val Ala Asp
20 25 30
Gly Ser Ser Lys Phe Pro His Gly Asp Phe Asn Val His Ala Val Cys
35 40 45
Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile
50 55 60
Gln Tyr Gly Glu Pro Phe Phe Ala Arg Tyr Pro Asn Gly Ile Ser His
65 70 75 80
Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Ser Ile Asp Arg Thr Val
85 90 95
Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu
100 105 110
Asp Gly Thr Cys Val Val Ser Arg Ile Thr Val Asn Cys Asp Gly Phe
115 120 125
Gln Pro Asp Gly Pro Ile Met Arg Asp Gln Leu Val Asp Ile Leu Pro
130 135 140
Asn Glu Thr His Met Phe Pro His Gly Pro Asn Ala Val Arg Gln Leu
145 150 155 160
Ala Phe Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His
165 170 175
Phe Asp Ser Lys Met Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro
180 185 190
Gly Pro His Phe Val Thr Thr Ile Thr Lys Gln Met Lys Asp Thr Ser
195 200 205
Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser
210 215 220
Val Pro Arg Ile Thr Ser Ala Ile
225 230